FIG. 1A

```
GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT      54
                                          Met Leu Ser Thr Ser
                                           1               5

CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC    102
Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr
                 10                  15                  20

ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG    150
Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val
             25                  30                  35

AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC    198
Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
         40                  45                  50

ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC    246
Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn
     55                  60                  65

TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC    294
Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala
 70                  75                  80                  85

ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT    342
Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser
                 90                  95                 100

GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA    390
Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr
             105                 110                 115

GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC    438
Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu
         120                 125                 130

CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA    486
Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu
     135                 140                 145
```

FIG. 1B

```
AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG      534
Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
150                 155                 160                 165

TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC      582
Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys
                170                 175                 180

CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA      630
Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly
            185                 190                 195

TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG      678
Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu
        200                 205                 210

CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG      726
Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu
    215                 220                 225

CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC      774
Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile
230                 235                 240                 245

TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT      822
Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile
                250                 255                 260

GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT      870
Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys
            265                 270                 275

GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT      918
Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu
        280                 285                 290

GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG      966
Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly
    295                 300                 305
```

FIG. 1C

```
GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC          1014
Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala
310                 315                 320                 325

CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG          1062
Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys
                330                 335                 340

AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA          1110
Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly
            345                 350                 355

AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA          1158
Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly
        360                 365                 370

GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC               1121
Ala

ACAGATGTGT GATTCACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG        1271

AGGAGAGAGA CTCCAGCTGG GTTGGAAAAC AGTATTTTCC AAACTACCTT CCAGTTCCTC        1331

ATTTTTGAAT ACAGGCATAG AGTTCAGACT TTTTTTAAAT AGTAAAAATA AAATTAAAGC        1391

TGAAAACTGC AACTTGTAAA TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG        1451

TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG        1511

GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA        1571

GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT        1631

TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT        1691

GCTGCCAAAA GCCTTTTGTG TTTTGTTTTG TATCATTATG AAGTCATGCG TTTAATCACA        1751

TTCGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA        1811

GTGGGAACTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAAACCCTA TTGGTAAAGA        1871
```

FIG. 1D

```
ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT   1931
AAGAATGTTC TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC   1991
TTCTAGAACC AGGCAACTTG GGAACTAGAC TCCCAAGCTG GACTATGGCT CTACTTTCAG   2051
GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA   2111
TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA   2171
TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA   2231
G                                                                   2232
```

FIG. 2A

```
CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT   60

TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC      110
                      Met Leu Ser Thr Ser Arg Ser Arg Phe Ile
                       1               5                  10

AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT    158
Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr
                 15                  20                  25

GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC    206
Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala
            30                  35                  40

CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG    254
Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val
        45                  50                  55

GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG    302
Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys
    60                  65                  70

TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT    350
Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu
75                  80                  85                  90

TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG    398
Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp
                 95                  100                 105

GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC    446
Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile
            110                 115                 120

GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA    494
Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg
        125                 130                 135

TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC    542
Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val
    140                 145                 150
```

FIG. 2B

```
ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT   590
Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe
155                 160                 165                 170

GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT   638
Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser
                175                 180                 185

GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC   686
Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His
            190                 195                 200

ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG   734
Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met
        205                 210                 215

GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC   782
Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn
    220                 225                 230

GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT   830
Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile
235                 240                 245                 250

GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC   878
Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn
                255                 260                 265

ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA   926
Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln
            270                 275                 280

CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC   974
Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys
        285                 290                 295

TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG  1022
Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg
    300                 305                 310
```

FIG. 2C

TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA 1070
Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys
315 320 325 330

CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA 1118
Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr
335 340 345

AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA 1160
Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu
350 355 360

TAAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA 1220

CAAACTTCAA GGGTTTGTTG AACAATAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG 1280

GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA 1340

TAATCCAGAA AAACTGTGGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG 1400

AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTTCTAG TCTTCATAAT TTCTTCACTC 1460

AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG 1520

TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG 1580

GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT 1640

CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTTAA CCTTGAAGGG 1700

TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTGG TGGAGTCCGA 1760

TGATTCTCTT TTGCATAAGT GCATGACATA TTTTTGCTTT ATTACAGTTT ATCTATGGCA 1820

CCCATGCACC TTACATTTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT 1880

AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTTGT TTATAAAAGA TGCATTATCT 1940

ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG 1979

FIG. 3(A)

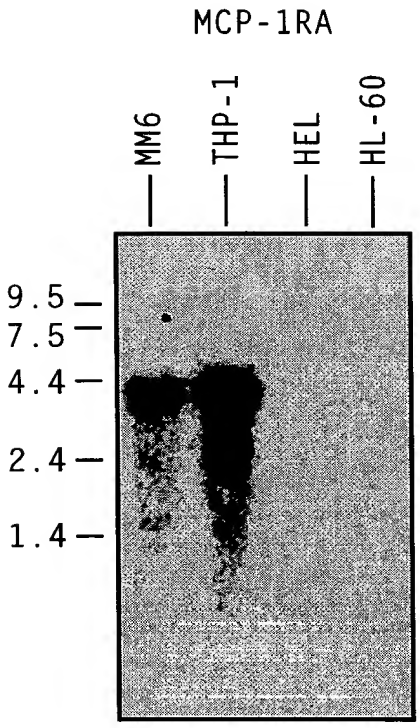


FIG. 3(B)

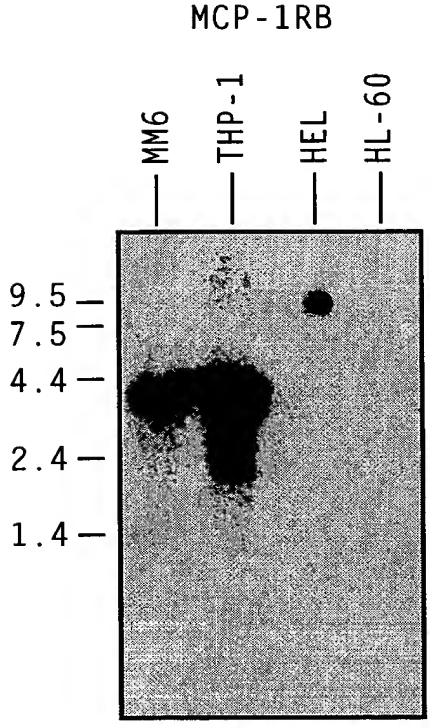


FIG.4(A)

```
                                                                                 
MCP-1RA  (CCR2-A)   MLSTSRSRFIRNTNESGEEVTTFFDYDYG--APCHKFDVKQIGAQLLPPL   48
MIP-1α/RANTESR      M----------ETPNTTEDYDTTTEFDYGDATPCQKVNERAFGAQLLPPL   40
HUMSTSR             MEGIS----IYTSDNYTEEMGS-GDYDSMK-EPCFREENANFNKIFLPTI   44
IL-8RA              MSNITDPQ-MWDFDDLNFTGMPPADEDY---SPC-MLETETLNKYVVIIA   45
IL-8RB              MESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVII   49

                    48       1       69        79       2
MCP-1RA  (CCR2-A)   YSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLW   98
MIP-1α/RANTESR      YSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLFTLPFW   90
HUMSTSR             YSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFW   94
IL-8RA              YALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIW   95
IL-8RB              YALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIW   99

                    101             115      3        136
MCP-1RA  (CCR2-A)   AH-SAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVF   147
MIP-1α/RANTESR      IDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFIILLTIDRYLAIVHAVF   140
HUMSTSR             AV-DAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATN   143
IL-8RA              AA-SKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHATR   144
IL-8RB              AA-SKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHATR   148

                          154       4         178
MCP-1RA  (CCR2-A)   ALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP--   195
MIP-1α/RANTESR      ALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTCSLHFPHE   190
HUMSTSR             SQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYPN-   192
IL-8RA              TLTQKR-HLVKFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEVLGN   193
IL-8RB              TLTQKRYLVKFI-CLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDMGN   197

                          204        5          231
MCP-1RA  (CCR2-A)   --RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVR   243
MIP-1α/RANTESR      SLREWKLFQALKLNLFGLVLPLLVMIICYTGIIKILLRRPNEKKS-KAVR   239
HUMSTSR             --DLWVVVFQFQHIMVGLILPGIVILFCYCIIISKLSHSKGHQKR-KALK   239
IL-8RA              DTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQK-HRAMR   242
IL-8RB              NTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ-KHRAMR   246

                    244         6         268
MCP-1RA  (CCR2-A)   VIFTIMIVYFLFWTPYNIVILLNTFQEF-FGLSNCESTSQLDQATQVTET   292
MIP-1α/RANTESR      LIFVIMIIFFLFWTPYNLTILISVFQDF-LFTHECEQSRHLDLAVQVTEV   288
HUMSTSR             TTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEA   289
IL-8RA              VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNNIGRALDATEI   292
IL-8RB              VIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI   296
```

FIG. 4(B)

```
                      295      7      313
                      ___________________*
MCP-1RA (CCR2-A)    LGMTHCCINPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKN  342
MIP-1α/RANTESR      IAYTHCCVNPVIYAFVGERFRKYLRQLFHRRVA-----------VHLVKW  327
HUMSTSR             LAFFHCCLNPILYAFLGAKFKTSAQHALTS--------------VSRGSS  325
IL-8RA              LGFLHSCLNPIIYAFIGQNFRHGFLKILA---------------MHGLVS  327
IL-8RB              LGILHSCLNPLIYAFIGQKFRHGLLKILAIH---------------GLIS  331

MCP-1RA (CCR2-A)    VKVTTQGLLDGRGKGKSIGRAPEASLQDKEGA                    374
MIP-1α/RANTESR      LPFLSVDRLE-RVSSTS-PSTGEHEL--SAGF                    355
HUMSTSR             LKILSKGK---RGGHSSVSTESESSS--FHSS                    352
IL-8RA              KEFLARH----RVTSYT-SSSVNVS----SNL                    350
IL-8RB              KDSLPKDS---RPSFVG-SSSGHTS----TTL                    355
```

FIG. 5

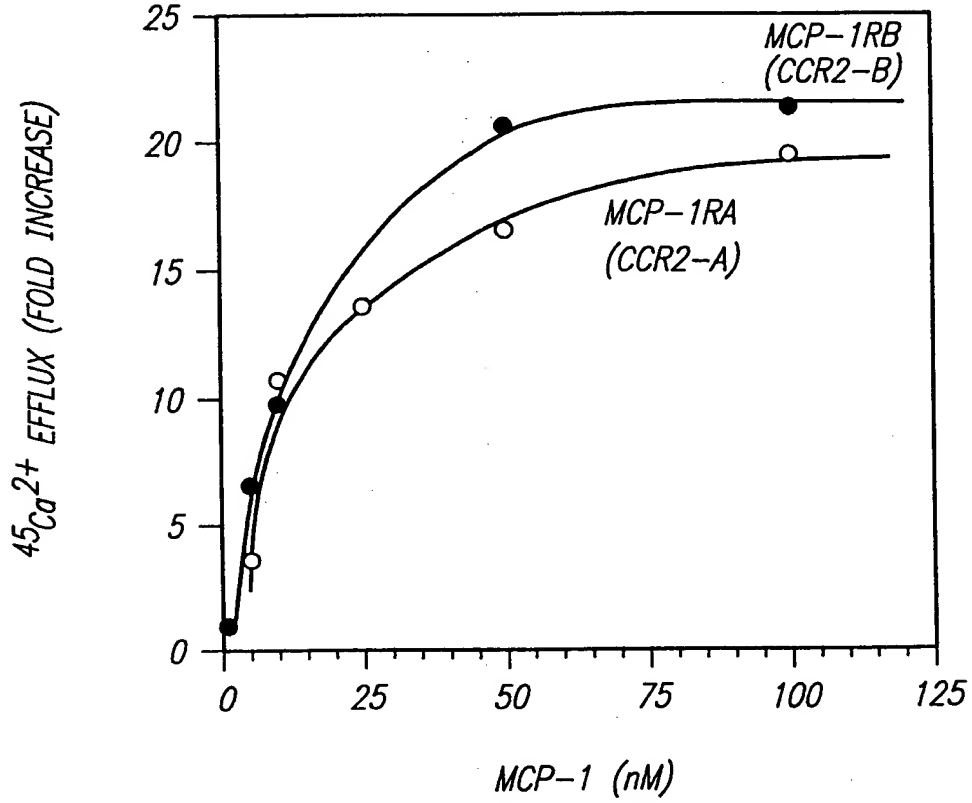


FIG. 6

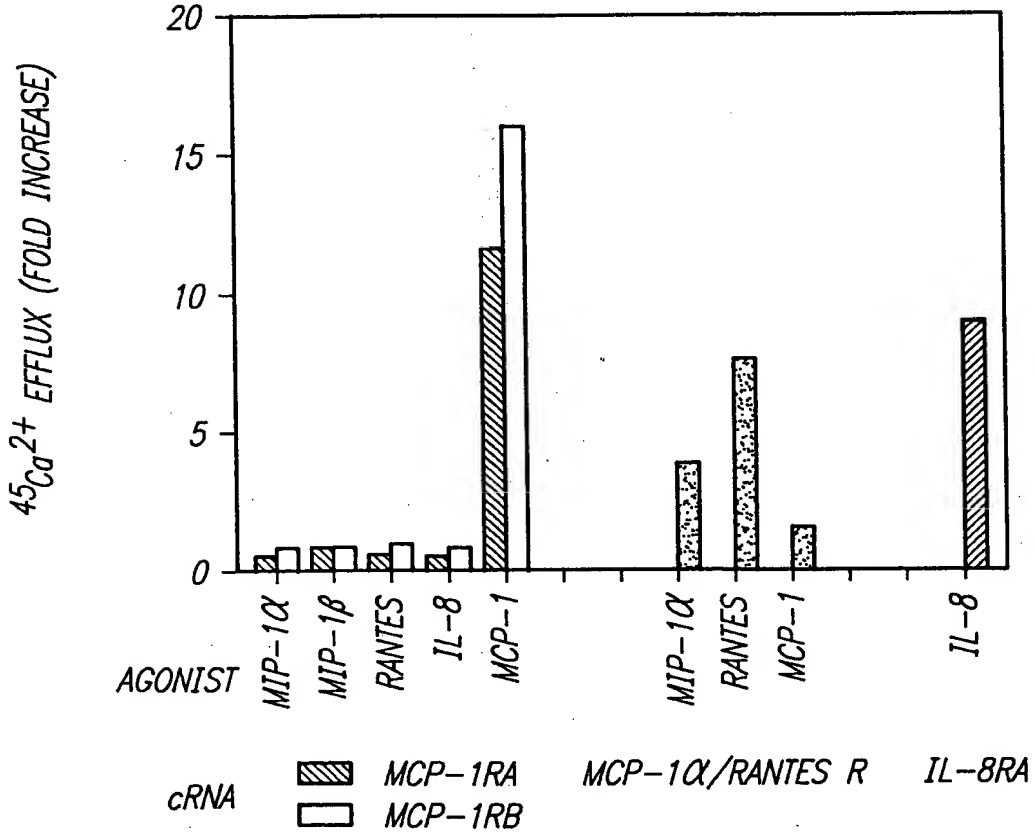


FIG. 7A

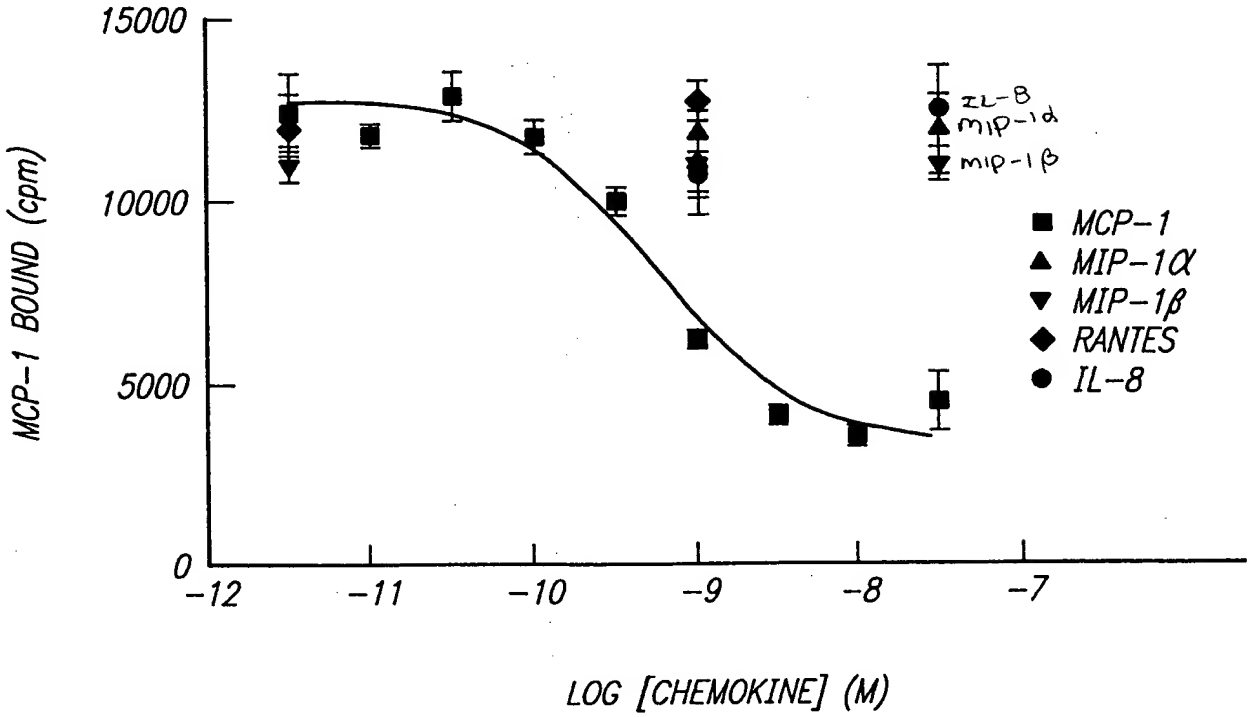
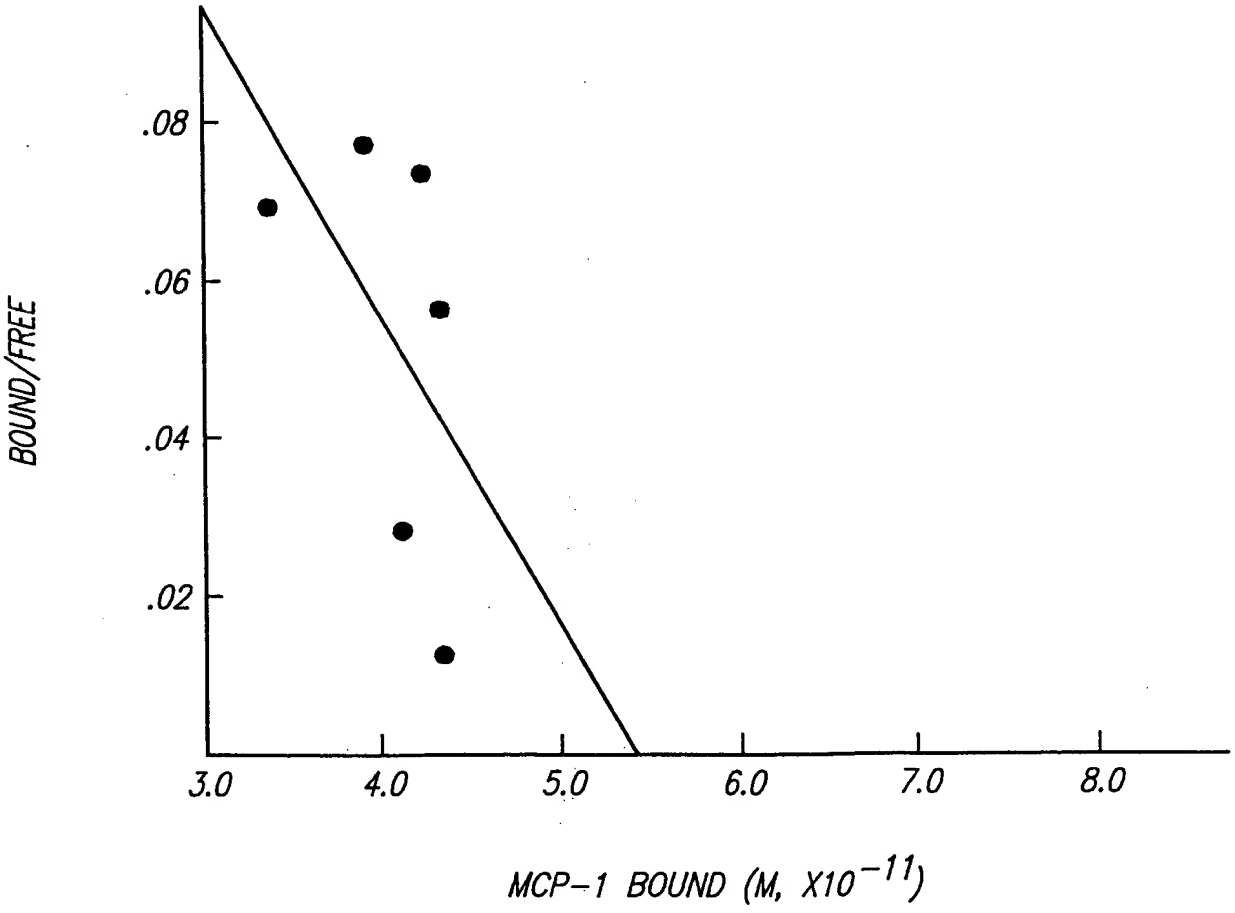


FIG. 7B



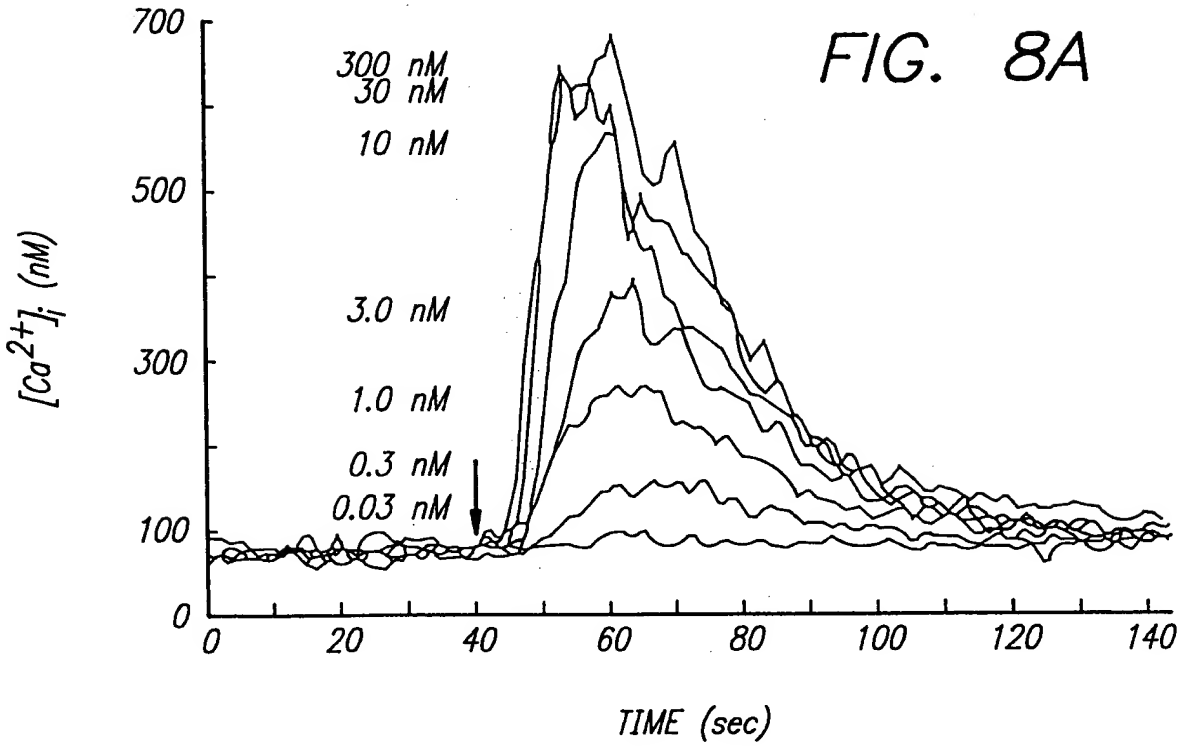


FIG. 8A

FIG. 8B

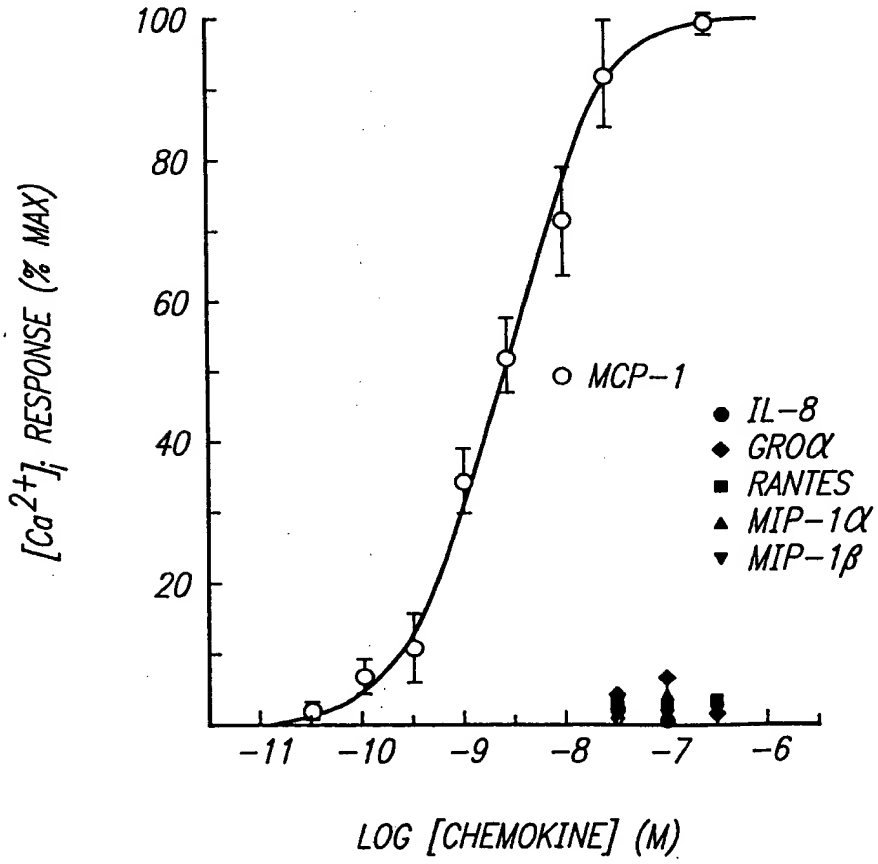


FIG. 8C